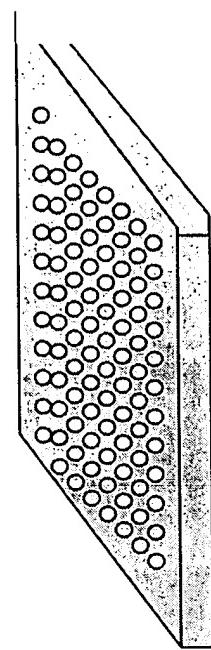
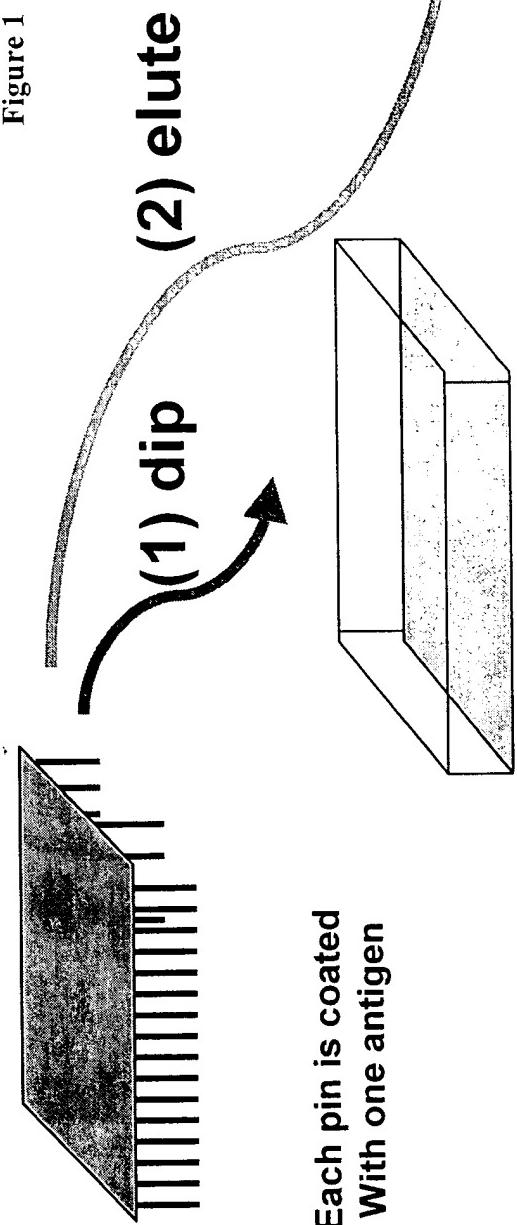


Figure 1



## **“Epitope Scan” over the extracellular domain of a receptor**

Figure 2

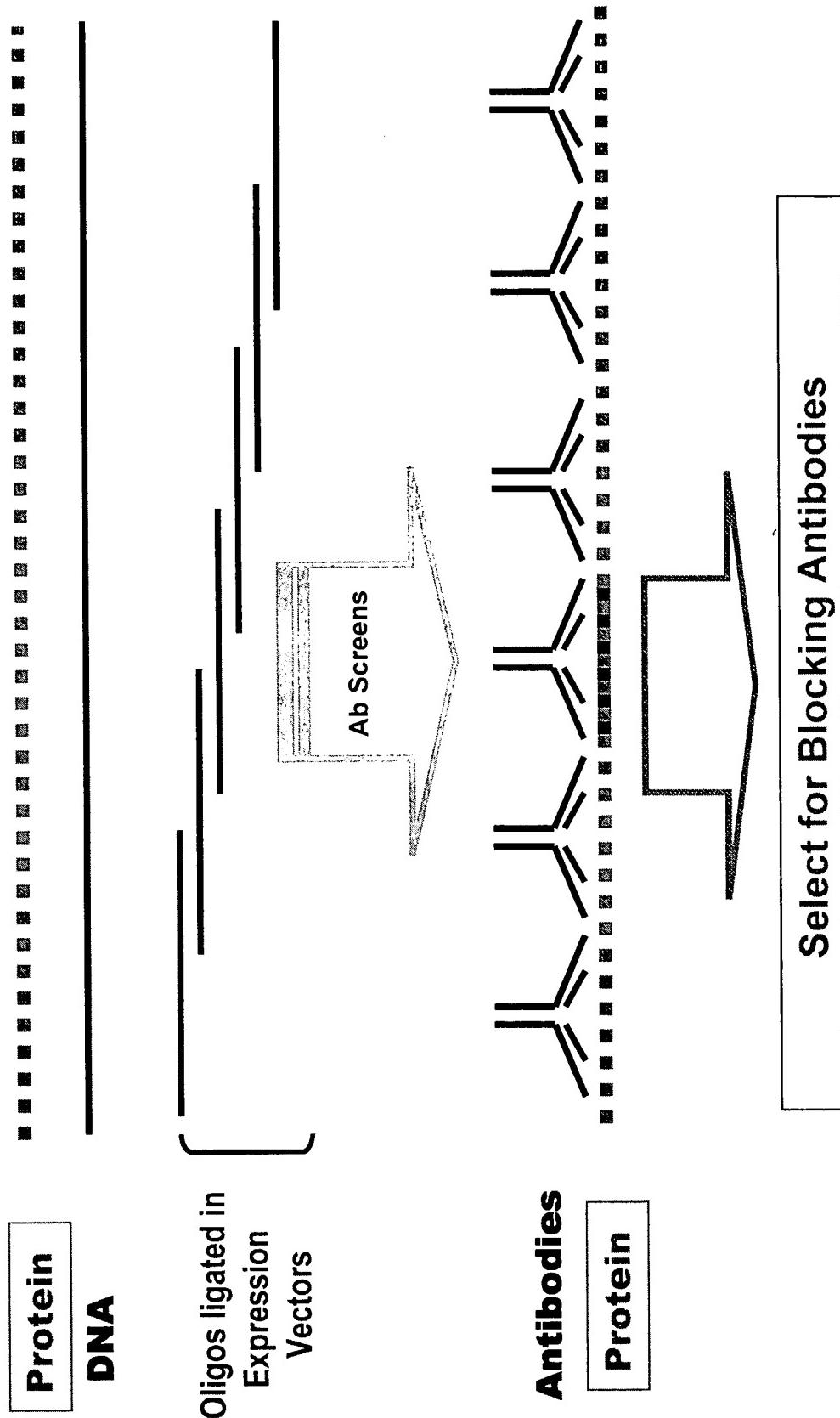
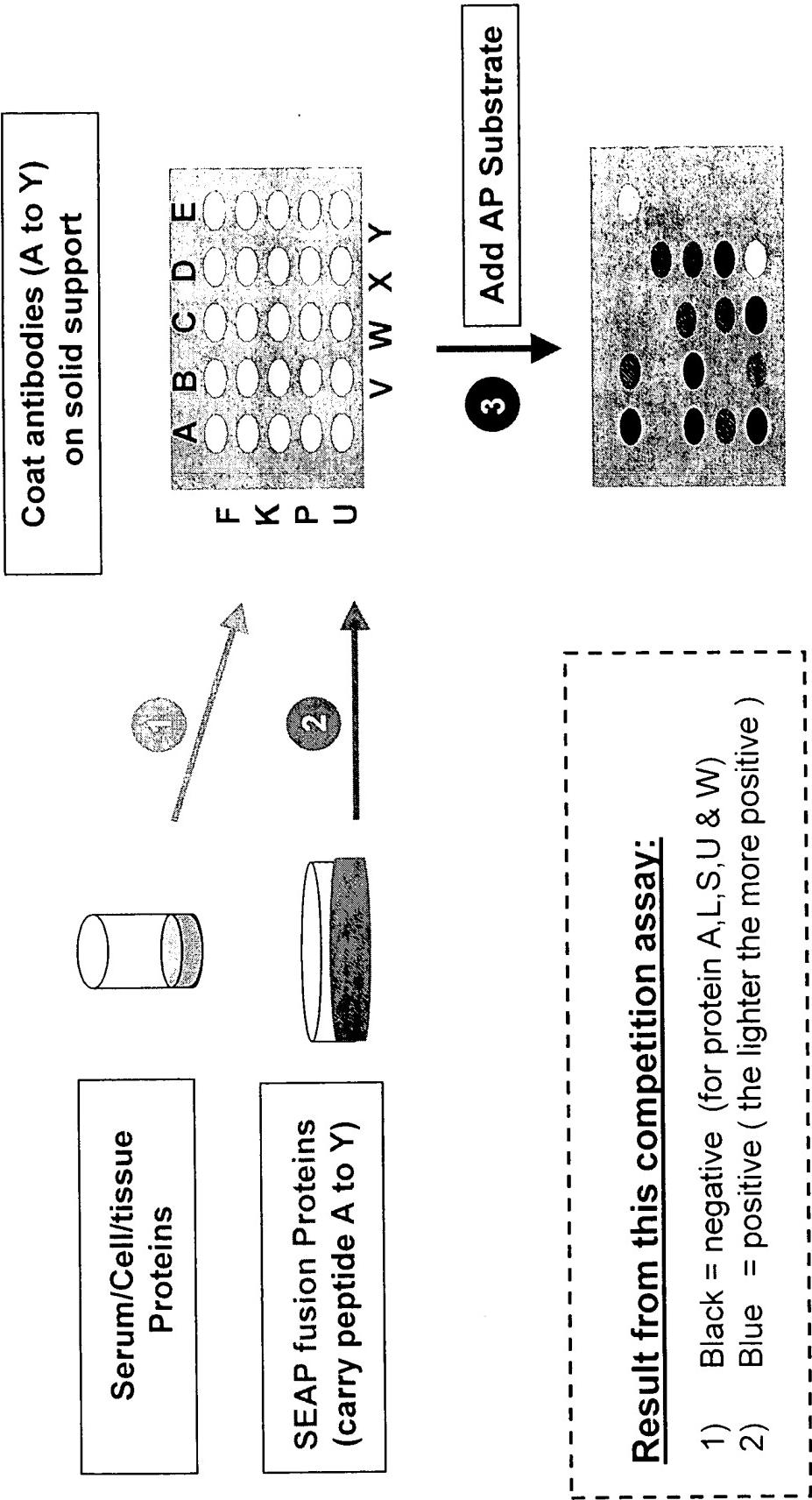


Figure 3



## FIGURE 4

### VEGF ISOFORM ALIGNMENT (VEGF-206, -165, -121)

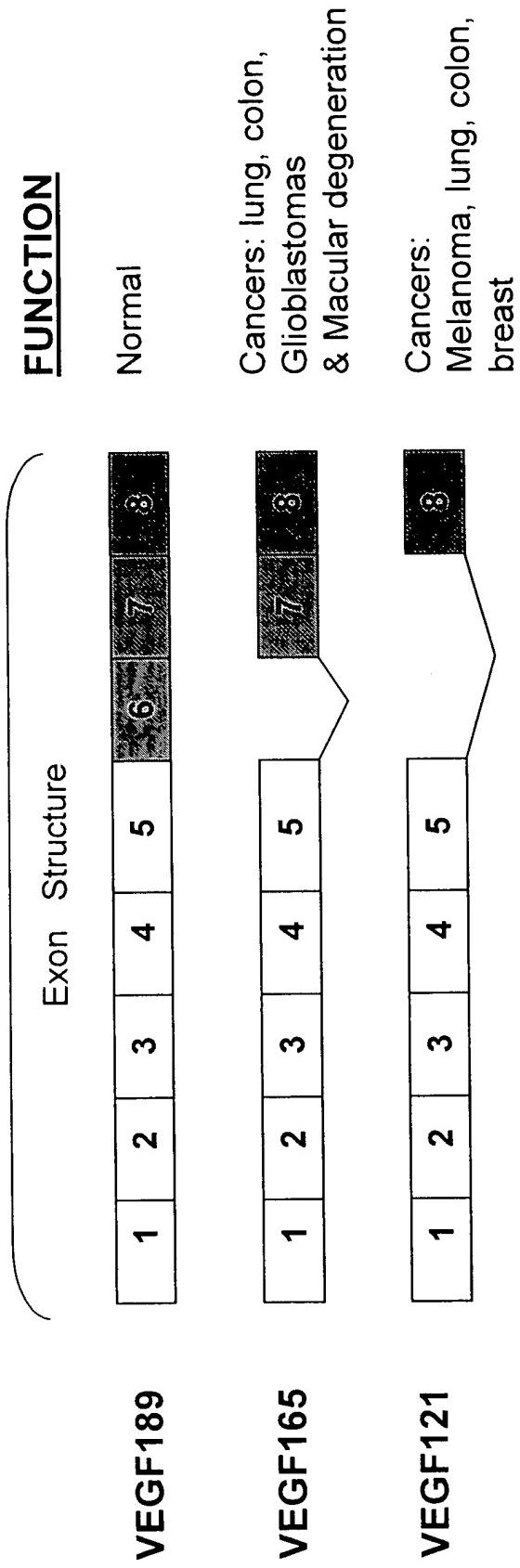
VEGF206 = (232-26)

VEGF165 = (191-26) Missing Exon 6

VEGF121 = (147-26) Missing Exon 6 + 7

SIGNAL PEPTIDE 1-26	<u>ISOFORM</u>
MNFLLSWVHW SLALLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD	206
MNFLLSWVHW SLALLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD	165
MNFLLSWVHW SLALLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD	121
ANTIBODY A4.6.1 EPITOPE REGION	
IFQEYPDEIE YIFKPSCVPL MRCGGCCNDE GLECVPTEES NITMQIMRIK PHQQHIGEM	206
IFQEYPDEIE YIFKPSCVPL MRCGGCSNDE GLECVPTEES NITMQIMRIK PHQQHIGEM	165
IFQEYPDEIE YIFKPSCVPL MRCGGCCNDE GLECVPTEES NITMQIMRIK PHQQHIGEM	121
HEPARIN BINDING DOMAIN	
PHPCGPCSER RKHLFVQDPQ TCKCSCKNTD SRCKARQLEL NERTCRCDKP RR	206
NPCGPCSER RKHLFVQDPQ TCKCSCKNTD SRCKARQLEL NERTCRCDKP RR	165
	KCDKP RR
	121

**Figure 5**



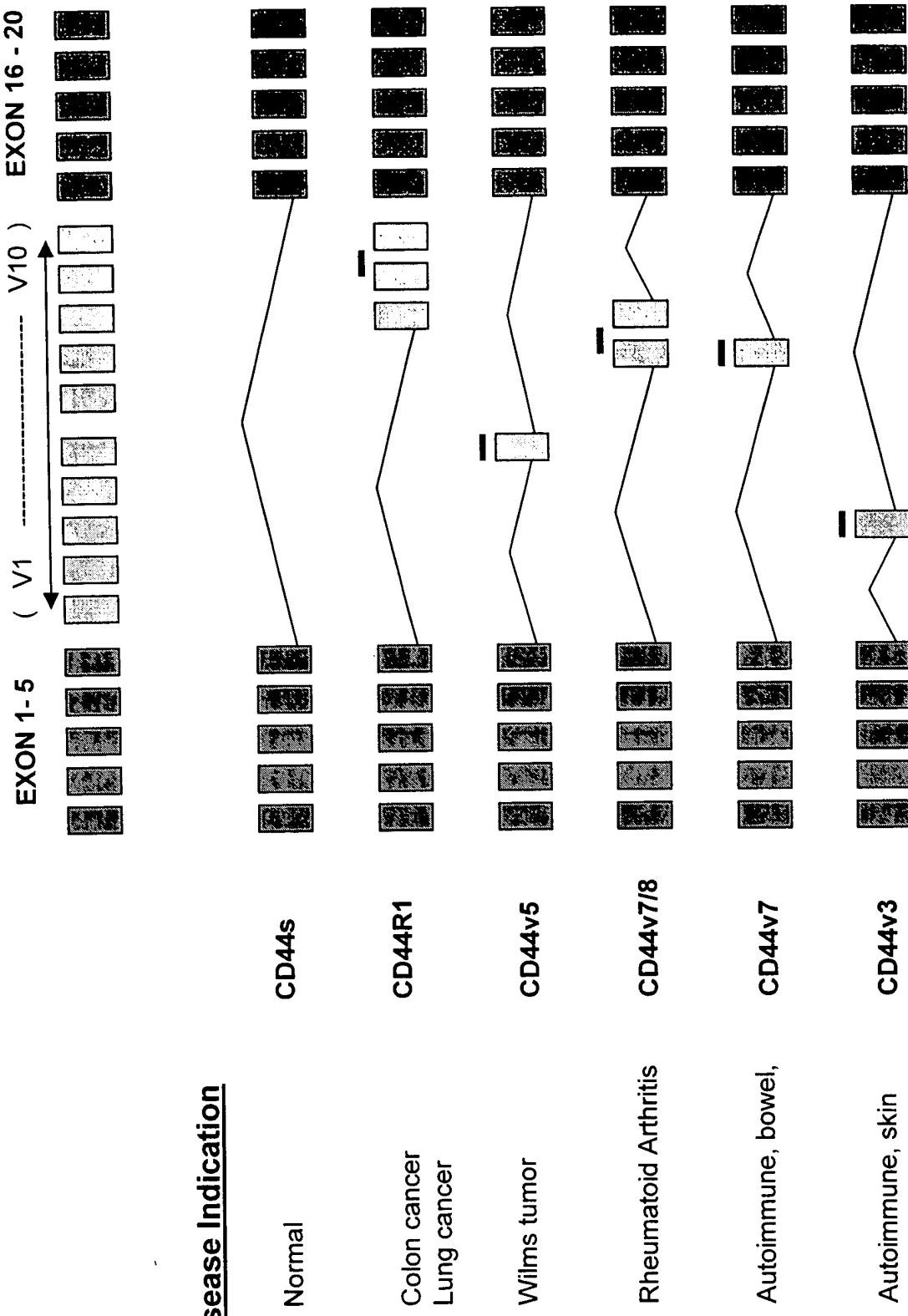
## SPECIFIC EPITOPES FOR VEGF ISOFORMS



**Anti-VEGF121**  
 for melanoma & breast cancer  
  
**Anti- VEGF165**  
 for glioblastoma

**Figure 6**

**Disease Indication**



**Figure 7A**

tcgcggaggc ttggggcagc cggtagctc ggaggtcg tg gcgcgtgggg ctagcaccag	60
cgcctgtcg ggaggcgcag cggttaggtg gaccggcag cgactcacc ggccaggcg	120
ctcgggtcg gaatttgata ttcattgatc cgggtttat cccttctt ttttcttaaa	180
catttttt taaaactgta ttgtttctcg ttttaattta ttttgcttg ccattcccc	240
cttgaatcg gccgacggct tggggagatt gctctacttc cccaaatcac tgtggattt	300
ggaaaccagc agaaagagga aagaggtgc aagagctcca gagagaagtc gaggaagaga	360
gagacggggt cagagagagc gcgcggcgt gcgagcagcg aaagcgacag gggcaaagt	420
agtgacctgc ttttgggggt gaccgccgga gcgcggcgtg agccctcccc ctggatcc	480
cgcagctgac cagtgcgcgt gacggacaga cagacagaca ccgcggccag cccagctac	540
cacccctcc ccggccggcg gcggacagtg gacgcggcgg cgagccgcgg gcagggccg	600
gagccgcgc ccggaggcgg ggtggagggg gtcggggctc gcggcgtcgc actgaaactt	660
ttcgtccaac ttctgggctg ttctcgcttc ggaggagccg tggccgcgc ggggaagcc	720
gagccgagcg gagccgcgag aagtgttagc tcggccggg aggagccca gcccggaggag	780
ggggaggagg aagaagagaa ggaagaggag agggggccgc agtggcact cggcgtcgg	840
aagccggcgt catggacggg tgaggcggcg gtgtgcgcag acagtgtcc agccgcgcgc	900
gctccccagg ccctggcccg gcctcgccgc cggggaggaa gagtagctcg ccgaggcgcc	960
gaggagagcg ggccggccca cagcccgagc cggagaggga gcgcgagccg cgccggcccc	1020
ggtcgggcct ccgaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc	1071
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser	
1 5 10	
ctt gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca	1119
Leu Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala	
15 20 25	
ccc atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc	1167
Pro Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe	
30 35 40	
atg gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg	1215
Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val	
45 50 55	
gac atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca	1263
Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro	
60 65 70 75	

**Figure 7B**

tcc tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly 80 85 90	1311
ctg gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met 95 100 105	1359
cgg atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu 110 115 120	1407
cag cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln 125 130 135	1455
gaa aaa aaa tca gtt cga gga aag gga aag ggg caa aaa cga aag cgc Glu Lys Lys Ser Val Arg Gly Lys Gly Lys Gln Lys Arg Lys Arg 140 145 150 155	1503
aag aaa tcc cgg tat aag tcc tgg agc gtt ccc tgt ggg cct tgc tca Lys Lys Ser Arg Tyr Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser 160 165 170	1551
gag cg <sup>g</sup> aga aag cat ttg ttt gta caa gat ccg cag acg tgt aaa tgt Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys 175 180 185	1599
tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag ctt gag tta Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu 190 195 200	1647
aac gaa cgt act tgc aga tgt gac aag ccg agg cgg tga gccgggcagg Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg 205 210 215	1696
aggaaggagc ctccctcagg gtttcgg	1723

**Figure 8A**

aattctcgag ctcgtcgacc ggtcgacgag ctcgagggtc gacgagctcg agggcgccgcg	60
ccccggccccc acccctcgca gcaccccgcg ccccgccccc tcccagccgg gtccagccgg	120
agccatgggg ccggagccgc agtgagcacc atg gag ctg gcg gcc ttg tgc cgc Met Glu Leu Ala Ala Leu Cys Arg	174
1 5	
tgg ggg ctc ctc ctc gcc ctc ttg ccc ccc gga gcc gcg agc acc caa Trp Gly Leu Leu Leu Ala Leu Leu Pro Pro Gly Ala Ala Ser Thr Gln	222
10 15 20	
gtg tgc acc ggc aca gac atg aag ctg cgg ctc cct gcc agt ccc gag Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu	270
25 30 35 40	
acc cac ctg gac atg ctc cgc cac ctc tac cag ggc tgc cag gtg gtg Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val	318
45 50 55	
cag gga aac ctg gaa ctc acc tac ctg ccc acc aat gcc agc ctg tcc Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser	366
60 65 70	
ttc ctg cag gat atc cag gag gtg cag ggc tac gtg ctc atc gct cac Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His	414
75 80 85	
aac caa gtg agg cag gtc cca ctg cag agg ctg cgg att gtg cga ggc Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly	462
90 95 100	
acc cag ctc ttt gag gac aac tat gcc ctg gcc gtg cta gac aat gga Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly	510
105 110 115 120	
gac ccg ctg aac aat acc acc cct gtc aca ggg gcc tcc cca gga ggc Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly	558
125 130 135	
ctg cgg gag ctg cag ctt cga agc ctc aca gag atc ttg aaa gga ggg Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly	606
140 145 150	
gtc ttg atc cag cgg aac ccc cag ctc tac cag gac acg att ttg Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu	654
155 160 165	
tgg aag gac atc ttc cac aag aac aac cag ctg gct ctc aca ctg ata Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile	702
170 175 180	

**Figure 8B**

gac acc aac cgc tct cg	g	cc	tgc cac ccc tgt tct ccg atg tgt aag	750
Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys				
185	190	195	200	
ggc tcc cgc tgc tgg gga gag agt tct gag gat tgt cag agc ctg acg	798			
Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr				
205	210	215		
cgc act gtc tgt gcc ggt ggc tgt gcc cgc tgc aag ggg cca ctg ccc	846			
Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro				
220	225	230		
act gac tgc tgc cat gag cag tgt gct gcc ggc tgc acg ggc ccc aag	894			
Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys				
235	240	245		
cac tct gac tgc ctg gcc tgc ctc cac ttc aac cac agt ggc atc tgt	942			
His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly Ile Cys				
250	255	260		
gag ctg cac tgc cca gcc ctg gtc acc tac aac aca gac acg ttt gag	990			
Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu				
265	270	275	280	
tcc atg ccc aat ccc gag ggc cgg tat aca ttc ggc gcc agc tgt gtg	1038			
Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val				
285	290	295		
act gcc tgt ccc tac aac tac ctt tct acg gac gtg gga tcc tgc acc	1086			
Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr				
300	305	310		
ctc gtc tgc ccc ctg cac aac caa gag gtg aca gca gag gat gga aca	1134			
Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr				
315	320	325		
cag cgg tgt gag aag tgc agc aag ccc tgt gcc cga gtg tgc tat ggt	1182			
Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly				
330	335	340		
ctg ggc atg gag cac ttg cga gag gtg agg gca gtt acc agt gcc aat	1230			
Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn				
345	350	355	360	
atc cag gag ttt gct ggc tgc aag aag atc ttt ggg agc ctg gca ttt	1278			
Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe				
365	370	375		
ctg ccg gag agc ttt gat ggg gac cca gcc tcc aac act gcc ccg ctc	1326			
Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu				
380	385	390		
cag cca gag cag ctc caa gtg ttt gag act ctg gaa gag atc aca ggt	1374			
Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly				
395	400	405		

**Figure 8C**

tac cta tac atc tca gca tgg ccg gac agc ctg cct gac ctc agc gtc Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val 410 415 420	1422
ttc cag aac ctg caa gta atc cg <sup>g</sup> gga cga att ctg cac aat ggc gcc Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala 425 430 435 440	1470
tac tcg ctg acc ctg caa ggg ctg ggc atc agc tgg ctg ggg ctg cgc Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg 445 450 455	1518
tca ctg agg gaa ctg ggc agt gga ctg gcc ctc atc cac cat aac acc Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr 460 465 470	1566
cac ctc tgc ttc gtg cac acg gtg ccc tgg gac cag ctc ttt cgg aac His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn 475 480 485	1614
ccg cac caa gct ctg ctc cac act gcc aac cgg cca gag gac gag tgt Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys 490 495 500	1662
gtg ggc gag ggc ctg gcc tgc cac cag ctg tgc gcc cga ggg cac tgc Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys 505 510 515 520	1710
tgg ggt cca ggg ccc acc cag tgt gtc aac tgc agc cag ttc ctt cgg Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg 525 530 535	1758
ggc cag gag tgc gtg gag gaa tgc cga gta ctg cag ggg ctc ccc agg Gly Gln Glu Cys Val Glu Cys Arg Val Leu Gln Gly Leu Pro Arg 540 545 550	1806
gag tat gtg aat gcc agg cac tgt ttg ccg tgc cac cct gag tgt cag Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln 555 560 565	1854
ccc cag aat ggc tca gtg acc tgt ttt gga ccg gag gct gac cag tgt Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys 570 575 580	1902
gtg gcc tgt gcc cac tat aag gac cct ccc ttc tgc gtg gcc cgc tgc Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys 585 590 595 600	1950
ccc agc ggt gtg aaa cct gac ctc tcc tac atg ccc atc tgg aag ttt Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe 605 610 615	1998

**Figure 8D**

cca gat gag gag ggc gca tgc cag cct tgc ccc atc aac tgc acc cac Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His 620 625 630	2046
tcc tgt gtg gac ctg gat gac aag ggc tgc ccc gcc gag cag aga gcc Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala 635 640 645	2094
agc cct ctg acg tcc atc gtc tct gcg gtg gtt ggc att ctg ctg gtc Ser Pro Leu Thr Ser Ile Val Ser Ala Val Val Gly Ile Leu Leu Val 650 655 660	2142
gtg gtc ttg ggg gtg gtc ttt ggg atc ctc atc aag cga cgg cag cag Val Val Leu Gly Val Val Phe Gly Ile Leu Ile Lys Arg Arg Gln Gln 665 670 675 680	2190
aag atc cgg aag tac acg atg cgg aga ctg ctg cag gaa acg gag ctg Lys Ile Arg Lys Tyr Thr Met Arg Arg Leu Leu Gln Glu Thr Glu Leu 685 690 695	2238
gtg gag ccg ctg aca cct acg gga gcg atg ccc aac cag gcg cag atg Val Glu Pro Leu Thr Pro Ser Gly Ala Met Pro Asn Gln Ala Gln Met 700 705 710	2286
cg <sup>g</sup> atc ctg aaa gag acg gag ctg agg aag gtg aag gtg ctt gga tct Arg Ile Leu Lys Glu Thr Glu Leu Arg Lys Val Lys Val Leu Gly Ser 715 720 725	2334
ggc gct ttt ggc aca gtc tac aag ggc atc tgg atc cct gat ggg gag Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu 730 735 740	2382
aat gtg aaa att cca gtg gcc atc aaa gtg ttg agg gaa aac aca tcc Asn Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg Glu Asn Thr Ser 745 750 755 760	2430
ccc aaa gcc aac aaa gaa atc tta gac gaa gca tac gtg atg gct ggt Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly 765 770 775	2478
gtg ggc tcc cca tat gtc tcc cgc ctt ctg ggc atc tgc ctg aca tcc Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser 780 785 790	2526
acg gtg cag ctg gtg aca cag ctt atg ccc tat ggc tgc ctc tta gac Thr Val Gln Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp 795 800 805	2574
cat gtc cgg gaa aac cgc gga cgc ctg ggc tcc cag gac ctg ctg aac His Val Arg Glu Asn Arg Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn 810 815 820	2622

**Figure 8E**

tgg tgt atg cag att gcc aag ggg atg agc tac ctg gag gat gtg cgg Trp Cys Met Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Asp Val Arg 825 830 835 840	2670
ctc gta cac agg gac ttg gcc gct cgg aac gtg ctg gtc aag agt ccc Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro 845 850 855	2718
aac cat gtc aaa att aca gac ttc ggg ctg gct cgg ctg gac att Asn His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile 860 865 870	2766
gac gag aca gag tac cat gca gat ggg ggc aag gtg ccc atc aag tgg Asp Glu Thr Glu Tyr His Ala Asp Gly Gly Lys Val Pro Ile Lys Trp 875 880 885	2814
atg gcg ctg gag tcc att ctc cgc cgg cgg ttc acc cac cag agt gat Met Ala Leu Glu Ser Ile Leu Arg Arg Arg Phe Thr His Gln Ser Asp 890 895 900	2862
gtg tgg agt tat ggt gtg act gtg tgg gag ctg atg act ttt ggg gcc Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala 905 910 915 920	2910
aaa cct tac gat ggg atc cca gcc cgg gag atc cct gac ctg ctg gaa Lys Pro Tyr Asp Gly Ile Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu 925 930 935	2958
aag ggg gag cgg ctg ccc cag ccc atc tgc acc att gat gtc tac Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr 940 945 950	3006
atg atc atg gtc aaa tgt tgg atg att gac tct gaa tgt cgg cca aga Met Ile Met Val Lys Cys Trp Met Ile Asp Ser Glu Cys Arg Pro Arg 955 960 965	3054
ttc cgg gag ttg gtg tct gaa ttc tcc cgc atg gcc agg gac ccc cag Phe Arg Glu Leu Val Ser Glu Phe Ser Arg Met Ala Arg Asp Pro Gln 970 975 980	3102
cgc ttt gtg gtc atc cag aat gag gac ttg ggc cca gcc agt ccc ttg Arg Phe Val Val Ile Gln Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu 985 990 995 1000	3150
gac agc acc ttc tac cgc tca ctg ctg gag gac gat gac atg ggg Asp Ser Thr Phe Tyr Arg Ser Leu Leu Glu Asp Asp Asp Met Gly 1005 1010 1015	3195
gac ctg gtg gat gct gag gag tat ctg gta ccc cag cag ggc ttc Asp Leu Val Asp Ala Glu Glu Tyr Leu Val Pro Gln Gln Gly Phe 1020 1025 1030	3240

**Figure 8F**

ttc tgt cca gac cct	gcc ccg ggc gct ggg	ggc atg gtc cac cac	3285
Phe Cys Pro Asp Pro	Ala Pro Gly Ala Gly	Gly Met Val His His	
1035	1040	1045	
agg cac cgc agc tca	tct acc agg agt ggc	ggt ggg gac ctg aca	3330
Arg His Arg Ser Ser	Ser Thr Arg Ser Gly	Gly Gly Asp Leu Thr	
1050	1055	1060	
cta ggg ctg gag ccc	tct gaa gag gag gcc	ccc agg tct cca ctg	3375
Leu Gly Leu Glu Pro	Ser Glu Glu Glu Ala	Pro Arg Ser Pro Leu	
1065	1070	1075	
gca ccc tcc gaa ggg	gct ggc tcc gat gta	ttt gat ggt gac ctg	3420
Ala Pro Ser Glu Gly	Ala Gly Ser Asp Val	Phe Asp Gly Asp Leu	
1080	1085	1090	
gga atg ggg gca gcc	aag ggg ctg caa agc	ctc ccc aca cat gac	3465
Gly Met Gly Ala Ala	Lys Gly Leu Gln Ser	Leu Pro Thr His Asp	
1095	1100	1105	
ccc agc cct cta cag	cgg tac agt gag gac	ccc aca gta ccc ctg	3510
Pro Ser Pro Leu Gln	Arg Tyr Ser Glu Asp	Pro Thr Val Pro Leu	
1110	1115	1120	
ccc tct gag act gat	ggc tac gtt gcc ccc	ctg acc tgc agc ccc	3555
Pro Ser Glu Thr Asp	Gly Tyr Val Ala Pro	Leu Thr Cys Ser Pro	
1125	1130	1135	
cag cct gaa tat gtg	aac cag cca gat gtt	cgg ccc cag ccc cct	3600
Gln Pro Glu Tyr Val	Asn Gln Pro Asp Val	Arg Pro Gln Pro Pro	
1140	1145	1150	
tcg ccc cga gag ggc	cct ctg cct gct gcc	cga cct gct ggt gcc	3645
Ser Pro Arg Glu Gly	Pro Leu Pro Ala Ala	Arg Pro Ala Gly Ala	
1155	1160	1165	
act ctg gaa agg gcc	aag act ctc tcc cca	ggg aag aat ggg gtc	3690
Thr Leu Glu Arg Ala	Lys Thr Leu Ser Pro	Gly Lys Asn Gly Val	
1170	1175	1180	
gtc aaa gac gtt ttt	gcc ttt ggg ggt gcc	gtg gag aac ccc gag	3735
Val Lys Asp Val Phe	Ala Phe Gly Gly Ala	Val Glu Asn Pro Glu	
1185	1190	1195	
tac ttg aca ccc cag	gga gga gct gcc cct	cag ccc cac cct cct	3780
Tyr Leu Thr Pro Gln	Gly Gly Ala Ala Pro	Gln Pro His Pro Pro	
1200	1205	1210	
cct gcc ttc agc cca	gcc ttc gac aac ctc	tat tac tgg gac cag	3825
Pro Ala Phe Ser Pro	Ala Phe Asp Asn Leu	Tyr Tyr Trp Asp Gln	
1215	1220	1225	

**Figure 8G**

gac cca cca gag cg <sup>g</sup> ggg gct cca ccc agc acc ttc aaa ggg aca Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr 1230 1235 1240	3870
cct acg gca gag aac cca gag tac ctg ggt ctg gac gtg cca gtg Pro Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val 1245 1250 1255	3915
tga accagaaggc caagtccgca qaagccctga tgtgtcctca gggagcaggg	3968
aaggcctgac ttctgctggc atcaagaggt gggagggccc tccgaccact tccaggggaa	4028
cctgccatgc caggaacctg tcctaaggaa cttcccttcc tgcttgagtt cccagatggc	4088
tggaaggggt ccagcctcg <sup>t</sup> tggaagagga acagcactgg ggagtcttg tggattctga	4148
ggccctgccc aatgagactc tagggtccag tggatgccac agcccagctt ggcccttcc	4208
ttccagatcc tgggtactga aagccttagg gaagctggcc tgagagggga agcggcccta	4268
agggagtg <sup>t</sup> taagaacaaa agcgacccat tcagagactg tccctgaaac ctagtactgc	4328
cccccatgag gaaggaacag caatggtgc agtatccagg ctttgtacag agtgctttc	4388
tgttagtt ttacttttt tgttttgttt tttaaagac gaaataaaga cccaggggag	4448
aatgggtgtt gtatggggag gcaagtgtgg ggggtccttc tccacaccca ctttgtccat	4508
ttgcaaataat attttggaaa ac	4530

**Figure 9A**

agcccccaagc ttaccacctg cacccggaga gctgtgtgc acc atg tgg gtc ccg Met Trp Val Pro 1	55
gtt gtc ttc ctc acc ctg tcc gtg acg tgg att ggt gct gca ccc ctc Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu 5 10 15 20	103
atc ctg tct cggtt att gtg gga ggc tgg gag tgc gag aag cat tcc caa Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln 25 30 35	151
ccc tgg cag gtg ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly 40 45 50	199
gtt ctg gtg cac ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg 55 60 65	247
aac aaa agc gtg atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu 70 75 80	295
gac aca ggc cag gta ttt cag gtc agc cac agc ttc cca cac ccg ctc Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu 85 90 95 100	343
tac gat atg agc ctc ctg aag aat cga ttc ctc agg cca ggt gat gac Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp 105 110 115	391
tcc agc cac gac ctc atg ctg ctc cgc ctg tca gag cct gcc gag ctc Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu 120 125 130	439
acg gat gct gtg aag gtc atg gac ctg ccc acc cag gag cca gca ctg Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu 135 140 145	487
ggg acc acc tgc tac gcc tca ggc tgg ggc agc att gaa cca gag gag Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu 150 155 160	535
ttc ttg acc cca aag aaa ctt cag tgt gtg gac ctc cat gtt att tcc Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His Val Ile Ser 165 170 175 180	583
aat gac gtg tgt gcg caa gtt cac cct cag aag gtg acc aag ttc atg Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr Lys Phe Met 185 190 195	631

**Figure 9B**

ctg tgt gct gga cgc tgg aca ggg ggc aaa agc acc tgc tcg ggt gat Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp 200 205 210	679
tct ggg ggc cca ctt gtc tgt aat ggt gtg ctt caa ggt atc acg tca Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser 215 220 225	727
tgg ggc agt gaa cca tgt gcc ctg ccc gaa agg cct tcc ctg tac acc Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr 230 235 240	775
aag gtg gtg cat tac cgg aag tgg atc aag gac acc atc gtg gcc aac Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn 245 250 255 260	823
ccc tga gcacccctat caaccccta ttgttagtaaa cttggAACCT tggAAATgac Pro	879
caggccaaga ctcaagcctc cccagttcta ctgaccttg tccttaggtg tgaggtccag ggttgctagg aaaagaaaatc agcagacaca ggtgttagacc agagtgttc ttaaatggtg taattttgtc ctctctgtgt cctggggaat actggccatg cctggagaca tatcactcaa tttctctgag gacacagata ggtgggggtg tctgtgttat ttgtgggta cagagatgaa agaggggtgg gatccacact gagagagtgg agagtgacat gtgctggaca ctgtccatga agcactgagc agaagctgga ggcacaacgc accagacact cacagcaagg atggagctga aaacataacc cactctgtcc tggaggcact gggaaAGCCTA gagaaggctg tgagccaagg agggagggtc ttcccttggc atggatgg gatgaagtaa ggagaggac tggACCCCT ggaagctgat tcactatggg gggaggtgta ttgaagtccct ccagacaacc ctcagatttg atgatttcct agtagaactc acagaaataa agagctgtta tactgtg	939 999 1059 1119 1179 1239 1299 1359 1419 1466